

Sequence Range: 1 to 5864

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>BgIII
10 20 30 40 50 60 70 80 90 100
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CTGCTAGCCCTCTAGAGGGCTAGGGGATACCAGCTGAGAGTCATGTTAGACGAGACTACGGCGTATCAATTCGGTCAATAGACGAGGAGCAACACACAA

>MfeI
110 120 130 140 150 160 170 180 190 200
GGAGGTCTGCTGAGTAGTCTCGCGAGCAAAATTTAAGCTACAACAAGGCGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGCG
CCTCCAGCGACTCATACGCGCTGCTTTTAAATTCGATGTTGTTCCGTTCCGAACTGGCTGTTAAGCTACTTCTTAGACGAATCCCAATCCGCAAAACGC

>SpeI
210 220 230 240 250 260 270 280 290 300
CTGCTTCGCGATGTAGCGGCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTATAGCCCATATA
GACGAAGCGCTACATCCCGGCTATATGCGCAACTGTAACTAATACTGATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATAT

>CMV_promoter
310 320 330 340 350 360 370 380 390 400
TGGAGTCTCGCGTTACATACTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATGACGTCAATAATGACGTATGTTCCCATAGT
ACCTCAAGCGCAATGTATTGAATGCCATTACCGGGCGGACCGACTGGCGGGTTCCTGGGGCGGGTAATGCAGTTATTACTGCATACAAGGGTATCA

410 420 430 440 450 460 470 480 490 500
AACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGACTATTTACGTAACAGTCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
TTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTGATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTACATAGTATACGGTTCATCGGG

>NdeI
510 520 530 540 550 560 570 580 590 600
CCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCA
GGATACTGCAGTTACTGCCATTACCGGGCGGACCGCTAATACGGGTCACTGACTGGAATACCCCTGAAAGGTGAACCGTCAATGTAGTGCATATCAAGT

610 620 630 640 650 660 670 680 690 700
TCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATGGCGTGGATAGCGGTTTGACTACCGGGGATTTCAGTCTCCACCCCATGACGTCAA
AGCGATAATGGTACCTACGCCAAACCGCTCATGTAGTTACCGGCACCTATCGCCAACTGAGTGCCTTAAAGGTTACAGGTTGGGTAACGTGAGTT

710 720 730 740 750 760 770 780 790 800
TGGGAGTTTGTGTTGGCACCACCAATCAACGGGACTTTCACAAATGTCGTAACACTCCGCCCCATTGACGCAATGGGCGGTAGGGTACGTTACGGTGGGAG
ACCTCAACACCAACCGTGGTTTGTAGTTCGCTGAAAGGTTTACAGCATTTGTGAGGCGGGSTAATCGGTTTACCCGCCATCCGCACATGCCACCCCTC

>SacI
810 820 830 840 850 860 870 880 890 900
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CAGATATATCTGCTCGAGAGACCGATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATCCCTCTGGGTTCGACGATCA

>Ecl136II
>T7_promoter
910 920 930 940 950 960 970 980 990 1000
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ATTCGAACGGCGGTGGTACCTTAACCTGAACCTAGAATAAATCAACGACGACGATGATCTCAAGTAAGAAGATTTTTGTGTCACCGGGGCGGTCTCTG
M D W T W I L F L V A A T R V H S>
SIGEY S K K P G G P G K S>
910 920 930 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_0 980 990 1000>
10 20 30 4.5 TO 437 OF SIGEY-WNVCHU* 70 80 90 100>
10 1 1 TO 54 OF SIGEY 40 50>

>HindIII
>Kozak_sequence
>HindIII_linker_{Split}
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
CGCGCCGTGAACATGCTGAAGCGCGGCATGCCCGCGTCTGAGCCTGATTGGCCTGAAGCGCGGCATGCTGAGCCTGATCGACGGCAAGGGCCCCATAC
GCGCGGCACTTGTACGACTTCGCGCGGTACGGGGCGCAGGACTCGGACTAACCGGACTTCGCGCGGTACGACTCGGACTAGCTGCGGTTCCCGGGGTATG
R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I>
WNVCHU*
1010 1020 1030 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_70 1080 1090 1100>
110 120 130 1.5 TO 437 OF SIGEY-WNVCHU* 170 180 190 200>

>SfiI
1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
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CGAAGCAGACCGGGGACCGGAAGAGCGGAGTGGCGTAACGGGGTGGCGCGGCGGACGACTGGCGACCGCGCGGCACTTGTTCGTCTGGCGGTA
R F V L A L L A F P R F T A I A P T R A V L D R W R G V N K Q T A M>
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FIG 7

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
GTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
CACGATGTCTCAAGAAGTTCCACCACGGATGTATGCCGATGTATCTCTCTGTCAATAACCATAGACGGGAGACGACTTCGGTCAATGGAAAGCCTTTTTC
4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
AGTTGGTAGCTCTTGATCCCGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA
TCAACCATCGAGAACTAGGCCGCTTTGTTTGGTGGCGACCATCGCCACAAAAAACAACGTTCTGTCGTCTAATGCGCGCTTTTTTTCCTAGAGTCTT
4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTTGGTCAATGAGATTATCAAAAAGGATCTTCACCTAGA
CTAGGAAACTAGAAAAAGATGCCAGACTGCGAGTCACTTGTCTTTGAGTGCAATTCCTAAAACAGTACTCTAATAGTTTTTCTAGAGTGGATCT
4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
TCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGGACACCTATCTC
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4910 4920 4930 4940 4950 4960 4970 4980 4990 5000
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TCGCTAGACAGATAAGCAAGTAGGTATCAACGGACTGAGGGGAGCAGCATCTATTGATGCTATGCCCTCCCGAATGGTAGACGGGGTCAGACGTTAC
5010 5020 5030 5040 5050 5060 5070 5080 5090 5100
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TATGGCGCTCTGGGTGCGAGTGGCGAGGTCTAAATAGTCGTTATTTGGTGGTGGCGCTTCCCGGCTCGCGCTCTACACGAGAGTTGAAATAGGCGGA
5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
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GGTAGGTCAGATAAATAACACGCGCTTCGATCTCATTCATCAAGCGGTCAATTATCAAAAGCGTTGCAACAGCGTAACGATGTCCGTAGACACACAG
5210 5220 5230 5240 5250 5260 5270 5280 5290 5300
ACGTCGCTCGTTGGTATGGCTTCAATCAGCTCCGCTTCCCAACGATCAAGGGGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTC
TGGGAGCAGCAAAACCATACCGAAGTAAGTCGAGGCCAAGGGTGTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAATCGAGGAAG
5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
GGTCTCCGATCGTTGTGAGAAAGTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATCTCTTACTGTCTATGCCATCCGTAAAGAT
CCAGGAGGCTAGCAACAGTCTTCAATCAACCGCGCTCAATAGTGAGTACCAATACCGCTCGTACGTATTAAAGAGATGACAGTACGGTAGGCATTCTA
5410 5420 5430 5440 5450 5460 5470 5480 5490 5500
GCTTTTCTGTGACTGGTGTAGTACTCAACCAAGTCAATCTGAGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCGGCGTCAATACGGGATAATACCGC
CGAAAGACACTGACCATCTATGAGTTGGTTCAGTAAGACTCTTATCACAATACGCGCTGGCTCAACGAGAACGGGCGCAGTTATGCCCTATTATGGCG
5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
GCCACATAGCAGAACTTTAAAGTGCTCATCATTTGGAAGAGCTTCTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCCGATGTAA
CGGTGTATCGTCTTGAATTTTTCAGGAGTAGTAACCTTTTGAAGAAGCCCCGCTTTTGAGAGTTCTTAGAATGGCGACAACCTTAGGTCAAGCTACATT
5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
CCCACTCGTGACCCCACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAA
GGGTGAGCACGTGGGTGACTAGAAAGTCGTAGAAATGAAAGTGGTCGCAAGACCCACTCGTTTGTGCTTCCGTTTACGGCGTTTTTCCCTTATT
5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
GGGCGACACGGAATGTTGAATACTCATACTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGACGGGATACATATTGAAATG
CCGCTGTGCTTTTACAACCTTATGATATGAGAAAGAAAGTTATAAATCTCGTAAATAGTCCCAATAACAGAGTACTCGCTATGTATAAACTTAC
5810 5820 5830 5840 5850 5860
TATTAGAAAAATAAACAAATAGGGGTTCGCGCACATTTCCCGCAAAAGTGCCACTGACGTC
ATAAATCTTTTATTGTTATCCCAAGGGCGGTGTAAGGGGCTTTTTCACGGTGGACTGCAG

